

Leu Ser Gly Val Thr Arg Ala Ser Ala Ile Glu Leu Ile Arg Ser Trp  
 260 265 270

Gly Ile Pro Val Arg Glu Glu Arg Ile Ser Ile Asp Glu Val Tyr Ala  
 275 280 285

Ala Ser Ala Arg Gly Glu Leu Thr Glu Val Phe Gly Thr Gly Thr Ala  
 290 295 300

Ala Val Val Thr Pro Val Gly Glu Leu Asn Ile His Gly Lys Thr Val  
 305 310 315 320

Ile Val Gly Asp Gly Gln Ile Gly Asp Leu Ser Lys Lys Leu Tyr Glu  
 325 330 335

Thr Ile Thr Asp Ile Gln Leu Gly Lys Val Lys Gly Pro Phe Asn Trp  
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Thr Val Glu Val  
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<210> 66  
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<212> DNA

<213> *Bacillus subtilis*

<220>

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<222> (1)..(1425)

<400> 66

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gaa aaa caa att gaa gca gat gtt tat tac gga att cag acg ctc cgt 96  
 Glu Lys Gln Ile Glu Ala Asp Val Tyr Tyr Gly Ile Gln Thr Leu Arg  
 20 25 30

gct tct gaa aat ttt ccg atc aca gga tac aaa atc cat gag gaa atg 144  
 Ala Ser Glu Asn Phe Pro Ile Thr Gly Tyr Lys Ile His Glu Glu Met  
 35 40 45

att aac gca ctg gcg att gtg aaa aaa gct gcg gct ctt gcc aac atg 192  
 Ile Asn Ala Leu Ala Ile Val Lys Lys Ala Ala Ala Leu Ala Asn Met  
 50 55 60

gac gtg aaa cgg ctg tat gaa gga att ggc caa gct atc gta caa gcc 240  
 Asp Val Lys Arg Leu Tyr Glu Gly Ile Gly Gln Ala Ile Val Gln Ala  
 65 70 75 80

gct gac gag att ctg gaa ggc aag tgg cac gat cag ttt atc gtc gat 288  
 Ala Asp Glu Ile Leu Glu Gly Lys Trp His Asp Gln Phe Ile Val Asp  
 85 90 95

ccg att cag ggc ggt gcc gga act tct atg aac atg aac gcg aat gag 336  
 Pro Ile Gln Gly Gly Ala Gly Thr Ser Met Asn Met Asn Ala Asn Glu  
 100 105 110

gtt atc gga aac cgg gcg ctt gaa atc atg gga cat aaa aag gga gat		384	
Val Ile Gly Asn Arg Ala Leu Glu Ile Met Gly His Lys Lys Gly Asp			
115	120	125	
tat atc cat tta agt cca aac aca cat gtg aac atg tca cag tct cag		432	
Tyr Ile His Leu Ser Pro Asn Thr His Val Asn Met Ser Gln Ser Gln			
130	135	140	
aac gat gtg ttc ccg act gct atc cat att tcc aca ttg aag ctc tta		480	
Asn Asp Val Phe Pro Thr Ala Ile His Ser Thr Leu Lys Leu Leu			
145	150	155	160
gaa aaa ctg ctg aaa aca atg gaa gat atg cat agt gtg ttt aaa caa		528	
Glu Lys Leu Leu Lys Thr Met Glu Asp Met His Ser Val Phe Lys Gln			
165	170	175	
aaa gca cag gag ttt cac tct gtt att aaa atg ggc cgg aca cac ctt		576	
Lys Ala Gln Glu Phe His Ser Val Ile Lys Met Gly Arg Thr His Leu			
180	185	190	
caa gat gcg gtt ccg atc cgt ctt ggc cag gaa ttc gaa gct tac agc		624	
Gln Asp Ala Val Pro Ile Arg Leu Gly Gln Glu Phe Glu Ala Tyr Ser			
195	200	205	
cgt gtt ctc gag cgt gat atc aaa cga atc aag caa tcg cgc cag cac		672	
Arg Val Leu Glu Arg Asp Ile Lys Arg Ile Lys Gln Ser Arg Gln His			
210	215	220	
ctg tat gaa gtc aac atg ggc gca act gct gtt ggt aca ggg ctg aac		720	
Leu Tyr Glu Val Asn Met Gly Ala Thr Ala Val Gly Thr Gly Leu Asn			
225	230	235	240
gct gat cct gaa tat atc aaa cag gta gta aag cac ctt gct gat att		768	
Ala Asp Pro Glu Tyr Ile Lys Gln Val Val Lys His Leu Ala Asp Ile			
245	250	255	
agc ggg ctt cct ctt gtc ggc gct gat cat ctt gtt gat gcg aca caa		816	
Ser Gly Leu Pro Leu Val Gly Ala Asp His Leu Val Asp Ala Thr Gln			
260	265	270	
aat aca gat gcc tat aca gag gta tca gct tca tta aaa gtc tgc atg		864	
Asn Thr Asp Ala Tyr Thr Glu Val Ser Ala Ser Leu Lys Val Cys Met			
275	280	285	
atg aac atg tcg aag atc gca aac gac ctg cgc tta atg gcg tcg gga		912	
Met Asn Met Ser Lys Ile Ala Asn Asp Leu Arg Leu Met Ala Ser Gly			
290	295	300	
ccg cgc gcc gga ctt gcg gaa att tct ctg cct gca cgt cag ccg ggt		960	
Pro Arg Ala Gly Leu Ala Glu Ile Ser Leu Pro Ala Arg Gln Pro Gly			
305	310	315	320
tca tct att atg ccg ggg aaa gtc aat ccg gtt atg gcg gag ctg atc		1008	
Ser Ser Ile Met Pro Gly Lys Val Asn Pro Val Met Ala Glu Leu Ile			
325	330	335	
aac caa att gcg ttc cag gtt atc gga aat gac aat aca atc tgc ctt		1056	
Asn Gln Ile Ala Phe Gln Val Ile Gly Asn Asp Asn Thr Ile Cys Leu			
340	345	350	
gct tca gaa gcc ggc cag ctt gag ttg aac gtc atg gag ccc gtg ctt		1104	

Trusted sequence

Ala Ser Glu Ala Gly Gln Leu Glu Leu Asn Val Met Glu Pro Val Leu  
 355 360 365

gtc ttt aat ttg ctt caa tcc atc agc atc atg aac aac ggc ttc cgt 1152  
 Val Phe Asn Leu Leu Gln Ser Ile Ser Ile Met Asn Asn Gly Phe Arg  
 370 375 380

tcg ttc act gac aac tgc tta aaa ggc att gaa gcc aac gaa aag cgt 1200  
 Ser Phe Thr Asp Asn Cys Leu Lys Gly Ile Glu Ala Asn Glu Lys Arg  
 385 390 395 400

atg aag caa tac gta gaa aaa agc gca ggc gtg atc aca gct gtc aat 1248  
 Met Lys Gln Tyr Val Glu Lys Ser Ala Gly Val Ile Thr Ala Val Asn  
 405 410 415

ccg cat ctt ggg tat gaa gcg gca gct aga att gcc agg gaa gca att 1296  
 Pro His Leu Gly Tyr Glu Ala Ala Arg Ile Ala Arg Glu Ala Ile  
 420 425 430

atg aca ggg caa tct gtc cgg gat ctt tgt ctg cag cat gat gtg ctg 1344  
 Met Thr Gly Gln Ser Val Arg Asp Leu Cys Leu Gln His Asp Val Leu  
 435 440 445

act gaa gaa gaa ttg gat att att tta aac cca tat gag atg acc aaa 1392  
 Thr Glu Glu Glu Leu Asp Ile Ile Leu Asn Pro Tyr Glu Met Thr Lys  
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cca ggt atc gca ggg aaa gaa cta tta gaa aaa taa 1428  
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<210> 67  
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 <213> *Bacillus subtilis*

<400> 67  
 Met Leu Asn Gly Gln Lys Glu Tyr Arg Val Glu Lys Asp Phe Leu Gly  
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Glu Lys Gln Ile Glu Ala Asp Val Tyr Tyr Gly Ile Gln Thr Leu Arg  
 20 25 30

Ala Ser Glu Asn Phe Pro Ile Thr Gly Tyr Lys Ile His Glu Glu Met  
 35 40 45

Ile Asn Ala Leu Ala Ile Val Lys Lys Ala Ala Ala Leu Ala Asn Met  
 50 55 60

Asp Val Lys Arg Leu Tyr Glu Gly Ile Gly Gln Ala Ile Val Gln Ala  
 65 70 75 80

Ala Asp Glu Ile Leu Glu Gly Lys Trp His Asp Gln Phe Ile Val Asp  
 85 90 95

Pro Ile Gln Gly Gly Ala Gly Thr Ser Met Asn Met Asn Ala Asn Glu  
 100 105 110

Val Ile Gly Asn Arg Ala Leu Glu Ile Met Gly His Lys Lys Gly Asp  
 115 120 125